

FIG. 1A

Input file ftnzb48h10; Output File ftnzb48h10.pat
Sequence length 3637

GTCGACCCACGGGTTCGGCACTCAACAAATGCCCTGCCCGTCTGACTGCACCGTCCCCGCCGCTGCCGCCGGGCC 79

CAAGGCCAAGTTCGAGGGGGCGTTGCCAACCGAACGGCACAGCCCTTGCCCCGGGACCCGAGGAGGTGAGCCGGCGC 158

P	G	L	A	L	W	L	C	A	V	L	C	A	S	A	R	G	G	S	24	
CCT	GGG	CTC	CTG	GCG	CTG	TGG	CTT	TGC	GCT	GTG	CTG	TGC	GCA	TCG	GCG	CGC	GGG	GGC	AGC	293
D	P	Q	P	G	P	G	R	P	A	C	P	A	P	C	H	C	Q	E	D	44
GAC	CCC	CAG	CCT	GGC	CCG	GGG	CGT	CCC	GCC	TGC	CCG	GCT	CCC	TGC	CAC	TGC	CAG	GAC	GAC	353
G	I	M	L	S	A	D	C	S	E	L	G	L	S	V	V	P	A	D	L	64
GGC	ATC	ATG	CTG	TCC	GCT	GAC	TGC	TCC	GAG	CTC	GGG	CTC	TCA	GTG	GTG	CCT	GCG	GAC	CTG	413
D	P	L	T	A	Y	L	D	L	S	M	N	N	L	T	E	L	Q	P	G	84
GAC	CCC	CTG	ACG	GCT	TAC	CTA	GAC	CTC	AGT	ATG	AAC	AAC	CTC	ACG	GAG	CTT	CAG	CCG	GGT	473
L	F	H	H	L	R	F	L	E	E	L	R	L	S	G	N	H	L	S	H	104
CTC	TTC	CAC	CAC	CTG	CGC	TTC	CTG	GAG	GAG	CTG	CGG	CTC	TCA	GGG	AAC	CAC	CTC	TCA	CAC	533
I	P	G	Q	A	F	S	G	L	H	S	L	K	I	L	M	L	Q	S	N	124
ATC	CCG	GGA	CAG	GCA	TTC	TCC	GGC	CAC	AGC	CAC	CAC	CAC	ATG	CTG	CAG	AGC	AAC	AAC	593	

FIG.1B

Q	L	R	G	I	P	A	E	A	L	W	E	L	P	S	L	Q	S	I	R	144
CAG	CTC	CGT	GGG	ATC	CCA	GCA	GAG	GCA	CTA	TGG	GAG	CTG	CCC	AGC	CTG	CAG	TCG	CTG	CGC	653
L	D	A	N	L	I	S	L	V	P	E	R	S	F	E	G	L	S	S	L	164
CTA	GAT	GCT	AAT	CTC	ATC	TCC	CTG	GTC	CCT	GAG	AGA	AGC	TTT	GAG	GGG	CTC	TCC	TCC	CTC	713
R	H	L	W	L	D	D	N	A	L	T	E	I	P	V	R	A	L	N	N	184
CGC	CAC	CTC	TGG	CTG	GAT	GAC	AAT	GCA	CTC	ACT	GAG	ATC	CCC	GTC	AGA	GCT	CTC	AAC	AAC	773
L	P	A	L	Q	A	M	T	L	A	L	N	H	I	R	H	I	P	D	Y	204
CTT	CCT	GCC	CTA	CAG	GCC	ATG	ACC	TTG	GCT	CTC	AAC	CAT	ATC	CGC	CAC	ATC	CCT	GAC	TAT	833
A	F	Q	N	L	T	S	L	V	V	L	H	L	H	N	N	R	I	Q	H	224
GCC	TTC	CAG	AAC	CTC	ACC	AGT	CTT	GTG	GTG	CTG	CAT	CTA	CAT	AAC	AAC	CGC	ATC	CAG	CAT	893
V	G	T	H	S	F	E	G	L	H	N	L	E	T	L	D	L	N	Y	H	244
GTG	GGG	ACC	CAC	AGC	TTC	GAG	GGG	CTG	CAC	AAI	CTG	GAG	ACA	CTA	GAC	CTG	AAC	TAT	AAT	953
E	L	Q	E	F	P	L	A	I	R	T	L	G	R	L	Q	E	L	G	F	264
GAG	CTG	CAG	GAG	TTC	CCC	TTG	GCT	ATC	CGG	ACC	CTG	GGC	AGG	CTG	CAG	GAA	TTC	GGT	TTC	1013
H	N	N	N	I	K	A	I	P	E	K	A	F	M	G	N	P	L	L	Q	284
CAT	AAC	AAC	AAC	ATC	AAG	GCT	ATC	CCA	GAG	AAA	GCC	TTC	ATG	GGC	AAC	CCT	CTC	CTG	CAG	1073
T	I	H	F	Y	D	N	P	I	Q	F	V	G	R	S	A	F	Q	Y	L	304
ACA	ATA	CAT	TTT	TAT	GAC	AAC	CCA	ATC	CAG	TTT	GTG	GGA	AGG	TCA	GCA	TTC	CAG	TAC	CTG	1133

FIG. 1C

S	K	L	H	T	L	S	L	N	G	A	T	D	I	Q	E	F	P	D	L	324
TCT	AAA	CTG	CAT	ACG	CTA	TCT	TTG	AAT	GGT	GCC	ACT	GAT	ATC	CAA	GAG	TTC	CCA	GAC	CTC	1193
K	G	T	T	S	L	E	I	L	T	L	T	R	A	G	I	R	L	L	P	344
AAA	GGC	ACC	ACT	AGC	CTG	GAG	ATC	CTG	ACC	CTG	ACC	CGT	GCG	GGC	ATC	AGA	CTG	CTC	CCA	1253
P	G	V	C	Q	Q	L	P	R	L	R	I	L	E	L	S	H	N	Q	I	364
CCG	CGA	GTG	TGC	CAA	CAG	CTG	CCT	AGG	CTC	CGA	ATC	CTG	GAG	CTG	TCT	CAT	AAT	CAG	ATC	1313
E	E	L	P	S	L	H	R	C	Q	K	L	E	E	I	G	L	R	H	N	384
GAG	GAG	TAA	CCC	AGC	CTG	CAC	AGA	TGT	CAG	AAG	CTG	GAG	GAA	ATT	GGC	CTC	CGA	CAT	AAC	1373
R	I	K	E	I	G	A	D	T	F	S	Q	L	G	S	L	Q	A	L	D	404
AGG	ATC	AAG	GAA	ATT	GGT	GCA	GAT	ACC	TTC	AGC	CAG	CTG	GGC	TCC	TTG	CAA	GCT	TTA	GAC	1433
L	S	W	N	A	I	R	A	I	H	P	E	A	F	S	T	L	R	S	L	424
CTG	AGT	TGG	AAT	GCC	ATC	CGT	GCC	ATC	CAC	CCT	GAG	GCT	TTC	TCA	ACC	CTT	CGA	TCC	TTG	1493
V	K	L	D	L	T	D	N	Q	L	T	T	L	P	L	A	G	L	G	G	444
GTT	AAG	CTG	GAC	CTG	ACT	GAC	AAAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGG	CTG	GGA	GGC	1553
L	M	H	L	K	L	K	G	N	L	A	L	S	Q	A	F	S	K	D	S	464
CTG	ATG	CAC	CTG	AAG	CTC	AAA	GGG	AAC	TTG	GCC	CTG	TCT	CAG	GCC	TTC	TCC	AAG	GAC	AGT	1613
F	P	R	L	R	I	L	E	V	P	Y	A	Y	Q	C	C	A	Y	G	I	484
TTC	CCA	AAA	CTG	AGG	ATC	CTG	GAG	GTG	CCC	TAC	GCC	TAC	CAG	TGC	TGT	GCC	TAC	GGC	ATC	1673

FIG. 1D

C	A	S	F	F	K	T	S	G	Q	W	Q	A	E	D	F	H	P	E	E	504
TGT	GCC	AGC	TTC	TTC	AAG	ACC	TCT	GGG	CAG	TGG	CAG	GCC	GAG	GAC	TTT	CAT	CCA	GAA	GAA	1733
E	E	A	P	K	R	P	L	G	L	L	A	G	Q	A	E	N	H	Y	D	524
GAG	GAG	GCA	CCA	AAG	AGG	CCC	CTG	GGT	CTC	CTT	GCT	GGA	CAA	GCT	GAG	AAC	CAC	TAT	GAC	1793
L	D	L	D	E	L	Q	M	G	T	E	D	S	K	P	N	P	S	V	Q	544
CTA	GAC	CTG	GAT	GAG	CTC	CAG	ATG	GGG	ACA	GAG	GAC	TCA	AAG	CCA	AAC	CCC	AGT	GTC	CAG	1853
C	S	P	V	P	G	P	F	K	P	C	E	H	L	F	E	S	W	G	I	564
TGC	AGC	CCT	GTT	CCA	GGC	CCC	TTC	AAG	CAC	TGC	GAG	CAC	CTC	TTT	GAG	AGC	TGG	GGC	ATC	1913
R	L	A	V	W	A	I	V	L	L	S	V	L	C	N	G	L	V	L	L	584
CGC	CTT	GCT	GTG	TGG	GCC	ATC	GTG	CTG	CTC	TCC	GTA	CTC	TGT	AAC	GGG	CTG	GTG	CTG	CTG	1973
T	V	F	A	S	G	P	S	P	L	S	P	V	K	L	V	V	G	A	M	604
ACA	GTC	TTT	GCC	AGC	GGA	CCC	AGC	CCG	CTG	TCC	CCC	GTC	AAG	CTT	GTG	GTG	GGT	GCG	ATG	2033
A	G	A	N	A	L	T	G	I	S	C	G	L	L	A	S	V	D	A	L	624
GCA	GGC	GCC	AAC	GCC	CTG	ACG	GGC	ATT	TCC	TGT	GGT	CTC	CTG	GCC	TCT	GTG	GAC	GCC	TTG	2093
T	Y	G	Q	F	A	E	Y	G	A	R	W	E	S	G	L	G	C	Q	A	644
ACC	TAT	GGT	CAG	TTC	GCT	GAG	TAT	GGA	GCC	CGC	TGG	GAG	AGC	GGT	CTG	GGC	TGC	CAG	GCT	2153
T	G	F	L	A	V	L	G	S	E	A	S	V	L	L	T	L	A	A	664	
ACG	GGC	TTC	CTG	GCT	GTC	CTG	GGT	TCA	GAG	GCG	TCG	CTG	CTC	ACA	CTG	GCG	GCC	2213		

FIG. 1E

V	Q	C	S	I	S	V	T	C	V	R	A	Y	G	K	A	P	S	P	G	684	
GTG	CAG	TGC	AGC	ATC	TCT	GTG	ACC	TGC	GTC	CGA	GCC	TAC	GGG	AAG	GCG	CCG	TCG	CCT	GGC	2273	
S	V	R	A	G	A	L	G	C	L	A	L	A	G	L	A	A	A	L	P	704	
AGC	GTC	CGC	GCA	GGC	GCA	CTG	GGA	TGC	CTG	GCG	CTG	GCC	GGG	CTG	GCC	GCA	GCA	CTG	CCG	2333	
L	A	S	V	G	E	Y	G	A	S	P	L	C	L	P	Y	A	P	P	E	724	
CTG	GCC	TCG	TCG	GGG	GAG	TAT	GGC	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCC	CCA	CCC	GAG	2393	
G	R	P	A	A	L	G	F	A	V	A	L	V	M	M	N	S	L	C	F	744	
GGC	CGG	CCG	GCC	GCC	CTG	GGC	TTC	GCT	GTC	GTA	GCC	CTG	GTG	ATG	ATG	AAC	TCG	CTC	TGC	TTC	2453
L	V	V	A	G	A	Y	I	K	L	Y	C	D	L	P	R	G	D	F	E	764	
CTG	GTG	GTG	GCC	GGC	GCC	TAC	ATC	AAG	CTC	TAC	TAC	TGT	GAC	CTG	CCA	CGG	GGT	GAC	TTT	GAG	2513
A	V	W	D	C	A	M	V	R	H	V	A	W	L	I	F	A	D	G	L	784	
GCC	GTG	TGG	GAC	TGC	GCC	ATG	GTG	CGC	CAC	GTG	GCC	TGG	CTC	ATC	TTT	GCA	GAT	GGC	CTC	2573	
L	Y	C	P	V	A	F	L	S	F	A	S	M	L	G	L	F	P	V	T	804	
CTC	TAC	TGC	CCC	GTG	GCC	TTC	CTC	AGC	TTT	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACC	2633	
P	E	A	V	K	S	V	L	L	V	V	L	P	L	P	A	C	L	N	P	824	
CCC	GAG	GCT	GTC	AAG	TCA	GTC	CTT	CTG	GTG	GTG	CTG	CTG	CCT	CTG	CCT	GCC	TGC	CTC	AAC	CCA	2693
L	L	Y	L	L	F	N	P	H	F	R	D	D	L	R	R	L	W	P	S	844	
CTG	CTC	TAC	CTG	CTC	TTC	AAC	CCT	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CTG	TGG	CCA	AGC	2753		

FIG. 1F

FIG. 1G

FIG. 2A

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
->nLeeLdLsnNKLtslppgalsnLpnLeeLdLsnNnLtslppg!fqnlk<-
+LdLs N+Lt+l pg+++++L+ Leel Ls+N+L+++p ++f++L+
ftmzb048h1
67 LTAYLDLSMNNLTELQPGFLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
->nLeeLdLsnNKLtslppgalsnLpnLeeLdLsnNnLtslppg!fqnlk<-
+L+ L L+ N+L++p++al+ Lp+L++L L+ N ++ +p++f++L+
ftmzb048h1
115 SLKILMLQSNQLRGIPAEALWEIPLSQLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
->nLeeLdLsnNKLtslppgalsnLpnLeeLdLsnNnLtslppg!fqnlk<-
+L++L+L++N Lt++p al+nLp L+ L N++f++p++fqnL+
ftmzb048h1
163 SLRHLWDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
->nLeeLdLsnNKLtslppgalsnLpnLeeLdLsnNnLtslppg!fqnlk<-
+L +L+L nN++f++ ++++++L+nLe+LdL++N+L++p + + L+
ftmzb048h1
211 SLVVLHLLHNNRIQHVGTHSFEGLHNLETLDLNYYNELQEFPL-AIRTLG 257

FIG.2B

RRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
->nLeelLsnNkLtslppgalsnLpnLeelLsnNnLtslppgffqnlk<-
+L+el + N+++ +p+ a+ + p L+ + +N ++ + ++fq L+
ftmzb048h1
258 RLQELGFHNNNIKAPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS 305

RRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
->nLeelLsnNkLtslppgalsnLpnLeelLsnNnLtslppgffqnlk<-
+L++L+L++ +++++p+ l++ ++Le L L + ++ lppg++q L+
ftmzb048h1
306 KLHTLSLNIGATdiQEFPD--LKGTTSLEIITLTRAGIRLLPPGVSQLP 352

RRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
->nLeelLsnNkLtslppgalsnLpnLeelLsnNnLtslppgffqnlk<-
+L+ L+Ls+N+++++p+ l+ ++Le+ L +N++++++ ++f+ L+
ftmzb048h1
353 RLRILELSHNQIEELPS-LHRCQKLEEIGLRLRNRIKEIGADTFSQLG 398

RRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
->nLeelLsnNkLtslppgalsnLpnLeelLsnNnLtslppgffqnlk<-
+L+ LdLs N ++ +p+a+s+L++L +LdL +N+Lt+lp + +L
ftmzb048h1
399 SLQALDLSWNRAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446

FIG. 3A-1

Protein (species)*	Function-lgand	Location
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm
Leucine-rich α 2-GP (human)	?-?	Serum
RNA1 (<i>Saccharomyces cerevisiae</i>)	RNA processing-?	Cytoplasm
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus
Biglycan (human)	ECM binding-laminin, fibronectin, TGF- β	ECM
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF- β	ECM
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM
Lumican (chicken)	Corneal transparency-?	ECM
Proteoglycan-Lb (chicken)	?-?	ECM
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM
Platelet GP ba (human)	Cell adhesion-WF, thrombin	PM (EC)
Platelet GP V (human)	Cell adhesion-GP IX, GP 1b	PM (EC)
YopM (<i>Yersinia pestis</i>)	Virulence factor-thrombin	TC + EC
IpaH7.8 (Shigella flexnen)	?-?	?
IpaH4.5 (Shigella flexnen)	?-?	?
Toll (Drosophilla)	Embryo development-?	PM (EC)
Silt (Drosophilla)	Axon development-?	EC
Connectin (Drosophilla)	Synapse development-?	PM (EC)
Chaoptin (Drosophilla)	Photoreceptor-cell development-?	PM (EC)
Flightless-1 (Drosophilla)	Embryo development-?	PM (EC)
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)

FIG. 3A-2

Repeats	Length	Consensus sequence	PIR entry
15	28 (A) 29 (B)	.LE.L.L..C-LT...C..L..aL... .L..EL.L..N-LGD.Ga..L..L..P..	A31857
8	24	.L..L..N..-L..LL...--. .L..L..N..-a...a..a...a... .L..L..a..N..-a..-...L--. .L..L..N..-I..-a...a...-..	NBHUA2 BVBYN1 S03616 A40757
8	29	.L..L..N..-a...a..a...a... .L..L..N..-I..-a...a...-..	
4	24	.L..L..N..-I..-a...a...-..	
8	24	.L..L..N..-I..-a...a...-..	
10	24	.L..L..N..-I..-V...a...-.. .L..L..N..-a...a...-..	NBHUC8
11	24	.L..L..N..-a...a...-..	S05390
12	24	.L..L..N..-L..-...a...-.. .L..a..L..N..-I..-...a...-.. .L..a..L..N..-a..-...F...-.. .L..L..N..-L..-LP..GL..-L--. .L..L..N..-L..-LP..LF..L--. .L..L..a..N..-L..-LP..-...L--PP	A41748 A41781 A35272 NBHUA -
6	24	.L..L..N..-L..-...a...-.. .L..a..N..-I..-...a...-.. .L..a..N..-L..-LP..-...L--P.	
6	24	.L..L..N..-L..-...a...-.. .L..a..N..-L..-LP..-...L--P.	
7	24	.L..L..N..-L..-LP..GL..-L--. .L..L..N..-L..-LP..LF..L--.	
14	24	.L..L..a..N..-L..-LP..-...L--PP	
12	20	.L..L..V..N..-L..-LP..-...L--P. .L..a..N..-L..-LP..-...L--P.	A33950 A35149 S18248
6	20	.L..L..N..-L..-...F...-.. .L..a..N..-L..-LP..-...L--P.	
8	20	.L..L..N..-L..-...F...-.. .L..a..N..-L..-LP..-...L--P.	
19	24	.L..L..N..-a..-a...F...a... .L..L..N..-I..-...F...L--. .L..L..N..-I..-a...aF..L--. .L..L..N..-a..-a...F...a... .L..L..N..-L..-aP..a..-L--. .L..L..L..N..-a..-a...L--.	A29943 A36665 S28464 A29944 -
7	24	.L..L..N..-a..-a...F...a... .L..L..N..-I..-...F...L--. .L..L..N..-I..-a...aF..L--.	
30	24	.L..L..N..-a..-a...F...a... .L..L..N..-I..-...F...L--. .L..L..N..-I..-a...aF..L--.	
16	23	.L..L..N..-a..-a...F...a... .L..L..N..-I..-...F...L--.	
8	24	.L..L..N..-a..-a...F...a... .L..L..N..-I..-...F...L--.	
			A34210

FIG. 3B-1

Protein (species)*	Function-lgand	Location
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)
Trk (human)	Receptor protein kinase-NGF	PM (EC)
TrkB (mouse)	Receptor protein kinase-BDNF,	PM (EC)
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)
LH-CG receptor (rat)	Signal transduction-LH, CG	PM (EC)
PSH receptor (rat)	Signal transduction-PSH	PM (EC)
TSH receptor (dog)	Signal transduction-TSH	PM (EC)
Adenylylate cyclase (Saccharomyces cerevisiae)	Signal transduction-RAS	PM (cytoplasm) ?
T-LR (Tyrpanosoma brucei)	?-?	Nucleus
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	?
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	?
DRT100 (Arabidopsis thaliana)	Recombination-?	Chloroplast
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoplasm
CCR4 (Saccharomyces cerevisiae)	Transcription-?	?
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	Nucleus
p34 ribosome-binding protein(rat)	RM membranes-ribosome	RM membrane (cytoplasm)
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma
Intermalin (Listeria monocytogenes)	Invasion-?	Cell wall
InIB (Listeria monocytogenes)	?-?	?
LRR superfamily		

FIG. 3B-2

Repeats	Length	Consensus sequence	PIR entry
8	27	.a..L..L..N---a...a...a...L---.	TDHUM4
2	23	.L..L..L..S..N..L..---.---.---.	TVHUTT
3	23	.L..L..aT..N..LTS..---.---.---T	S06943
3	23	.L..R..aNLSQN..L..S..---.---.---.	A40026
11	23	.L..a..L..N..G..aP..-a..SL--.	JQ1674
5	25	.L..L..a..T..a..F..---.	A41343
7	25	.L..L..aS..T..LP..a..a---.	A34548
6	25	.a..L..a..NN..a..S-a..a..a..---.	A40077
20	23	.L..L..L..N..a..-a..-a..L---.	0YBY
18	23	.L..L..L..LGGC..a..---a..-a..L---.	A36359
3	23	.a..L..a..DI..N--LP..a..N---.	DDBYD1
5	26	.L..L..a..C..a..a..a..a..---P	A25226
5	24	.L..LNL..N..L..G..IP..S-a..S---.	A46260
9	26	.L..a..L..C..N..ATD..a..-L..L..-.	A41529
4	23	.L..L..a..N..LT..-LP..E-a..---.	S31286
11	22	.L..L..a..N..I..-a--ENa..L---.	A38439
4	24	.L..LDL..N..L..-LP..F..L---.	-
12	24	.L..L..L..N..L..-LP..aF..L---.	A34901
13	22	NI..L..L..n-QISDI..P---L..L---T	A39930
6	22	.L..L..L..N..L..DI..---L..L---.	C39930
		5 10 15 20 25	
		.L..L..N*.a..*a***a**a**.**	

FIG. 4

>human DNA seq.

TAATACGACTCACTATAAGGGAAAGCTGGTACGCCTG .AGGTACCGGTCCGGAA
TTCGGGTCGACCCACGCGTCCGTGGAGCGGAGC CAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTGCTGCCCTAGCGGCCCT CAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCT CCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCCTGAGC CCTTCTCCACCCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTC ACCACACTGCCCTGGC
TGGACTTGGGGCTTGATGCATCTGAAGCTCAAAGC GAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTCCAAAAGTGGAGGA CCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGCCAGCT TCTCAAGGCCTCTGGG
CAGTGGGAGGGCTGAAGACCTTCACCTGATGATGAC GAGTCTTCAAAAAGGCC
CCTGGGCCTCCTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACAC CCACTGTCAGTGTAGC
CCTACTCCAGGCCCTCAAGCCCTGTGAGTACCTC TTTGAAAGCTGGGCAT
CCGCCTGGCCGTGTGGGCATCGTGTGCTCTCCG GCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTCGCTGGCAGGGCTGCCCCC CTGCCCCCGGTCAAGTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACI GGCATTTCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTGGTCAGTTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGCCACTGGCTTCCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGCAGCGTTCG
AGCAGGGGTCTAGGCTGCCACTGGCAGGGCTGGCGCCACTGCC
CTGGCCTCAGTGGGAGAATACGGGGCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTATGAT
GAACCTCTCTGTTCTGGTCGTGGCCGGTGCCTACATCAAACGTACTGTGA
CCTGCCGCAGGGCGACTTTGAGGCCGTGTGGACT GCGCCATGGTAGGGCAC
GTGGCCTGGCTCATTCGCAGACAGGGCTCCTCTACTGTCCCCTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTCCCTGTCACGCCGAGGCCGTCAAGT
CTGTCCTGCTGGTGGTGTGCTGCCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGATGACCTCAGGCCGGCTTCGGCCCCCGC
AGGGGACTCAGGGCCCTAGCCTATGCTGCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTCTGTATGTGGATCTATTCTG
GAAGCTTCTGAAGCTGGCGGCCCTGGCTGGAGACCTATGGCTTCCCTC
AGTGAACCTCATCTCTGTCAAGCAGCCAGGGCCCCAGGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGAAACCACTTGGGAACCCCCAACCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTG
TCAGGGGGTGGCGCTTCAAGCCCTCTGGCTTGGCCTTGCTTACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCTCTTCCC TTTCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCACTGACCTGGCTCCACTGATCACCTCTCCTGTGACCAT
CACCAACGGGTGCCCTTGGCCTGGCTTCCCTGGCCTCAGCTCACCT
TGATACTGGGCCTTCTGTGATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAATG TGTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAGACTTCCTATTAAAATAAGCTTGGAGAGATT
AAAAAAAAAAAAAGGGCGGCCGCTAGAGGATCAAGCTTACGTACCGT
GCATGCGACGTAGCTCTTATAGTGTACCTAAATTCAATT

FIG. 5

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAAALAASNTTASGKLE
DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPIAGLGLGMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEADLHLD
DEESSKRPPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAVWAVIPLLSQLCNGLVLLTVFAGGPAPLPPVKFWVGAIAGANTLTGISC
LLASVDALTFGQFSEYGARWETGLGC RATGFLAVLGSEASVLLTLAAVQCSVSVS
CVRAYGKSPSLGSVRAGVLGCLLAGLAALPLASVGEYGASPLCLPYAPP EGQP
AALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCA MVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLNFNPHFRDDL
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGEELLRAEGSTPAGGGL
SGGGFQPSGLAFASHV

FIG. 6

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11
*->nLeeLdLsnNKLtsppgalnLpnLeeLdLsnNnLtsppglfqnl
+L+LdLsN++s++p+a+s+L++L+LdL+N+Lt+P+L
fahr 64 SLQALDLSWNAAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGGL 110

K<-*

fahr 111 M 111

FIG. 7A

1	ftmzb048h10	MHSPPGLLALWLCAVILCASARGGSDPQPGRPACPA	CQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSMNNL	TE												
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~												
	fahr_human	~~~~~	~~~~~	~~~~~												
81	ftmzb048h10	LQPGLEHHRFLEELRLSGNHLSHIPGQAFSGLHS	LQSNQLRGIPAEALWELPSLQSLRILDANLISLVPERS	SEG												
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~												
	fahr_human	~~~~~	~~~~~	~~~~~												
161	ftmzb048h10	LSLRHLWDDNALTEIPVRA	LNLPALQAMTLAINH	HIRHIPDYAFQNLTSVVLHLHN	NRIQHVGTHS	FEGLHN	LETLD									
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~									
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~									
241	ftmzb048h10	INYNELQEFFPLAIRTIGRIQELGFHNNNIKA	PEKAFMGNPILLQ	TIHFYDNP1QFVGRSAFQYI	SKLHTLS	SINGATD	IQE									
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~									
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~									
321	ftmzb048h10	FPDLKGTTSL	EIITLTTRAGIRL	IPPGVCOQLP	RRILESHNQIEELPLSL	HRCQKLEEIG	GLRNRIKEIG	ADTFSQ	GSL							
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~							
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~							
401	ftmzb048h10	QALDLSWNAIRAIHPEAFSTLRS	LVKLDLTDNQLTTIPLAG	IGGIMHKL	KGNLALSQAFSKD	SFPLKRLILEV	PYAYQCC	481	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
	Fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
481	ftmzb048h10	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF							
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
560	ftmzb048h10	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF							
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
560	ftmzb048h10	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF							
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
80	ftmzb048h10	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF							
	Aa_of_aambb001d112	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF
	fahr_human	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	AYGICASFFKTS	GQWQAEDEHPEEEA	PKRPLGLI	AGQAENHYD	LDLDELQMGTEDSKP	NPSVQCS	PVPGPF	CEHLLF

FIG. 7B

<p>ftmzb048h10 Aa_of_aambb001d112 fahr_human</p> <p>ftmzb048h10 Aa_of_aambb001d112 fahr_human</p> <p>ftmzb048h10 Aa_of_aambb001d112 fahr_human</p>	<p>561 SWGIRLAVWAIVLLSVLCNGLVLILTVFAAGPSPLSPVKLUVVGAMAGANALTGQFQAEYGARWE SGL SWGIRLAVWAIVLLSVLCNGLVLILTVFAAGPSPLSPVKLUVVGAMAGANALSGQFQAEYGARWE SGL SWGIRLAVWAIVLLSVLCNGLVLILTVFAAGPSPLSPVKLUVVGAIAGANTLTGQFQSEYGARWE TGL</p> <p>640 SWGIRLAVWAIVLLSVLCNGLVLILTVFAAGPSPLSPVKLUVVGAMAGANALTGQFQAEYGARWE SGL SWGIRLAVWAIVLLSVLCNGLVLILTVFAAGPSPLSPVKLUVVGAMAGANALSGQFQAEYGARWE SGL SWGIRLAVWAIVLLSVLCNGLVLILTVFAAGPSPLSPVKLUVVGAIAGANTLTGQFQSEYGARWE TGL</p> <p>641 GCQATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY GCQATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY GCRATGFLAVLGSEASVLLLTLAAVQCSISVTCVRAYGKSPSLGSVRAGVLCCLALAGLAAALPLASVGEYGASPLCLPY</p>	<p>I</p> <p>TM II</p> <p>TM III</p> <p>TM IV</p> <p>TM V</p> <p>TM VI</p> <p>TM VII</p> <p>TM VIII</p> <p>TM IX</p>	<p>720 APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSFCFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL</p> <p>721 APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL</p> <p>722 APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL</p> <p>800 APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL APPGRPAALGEAVALVMMNSLCLFLVVGAYIKLYCDLPRGDFEAVWDCCAMVRHVAWLIFADGLLYCPVAFILSFASMLGL</p> <p>801 FPVTPEAVKSVLVLVPLPACLNPLLYLFLNPHEFRDDLRLRIWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL FPVTPEAVKSVLVLVPLPACLNPLLYLFLNPHEFRDDLRLRIWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL FPVTPEAVKSVLVLVPLPACLNPLLYLFLNPHEFRDDLRLRIWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL</p> <p>881 EASEAGQPPGLETYGPSPVTLISRHQPGATRLEGNHFIESDGTKEGNPQPPMKGELLLKAEGATLAGCGSSVGGALWPSG EASEAGQPPGLETYGPSPVTLISRHQPGATRLEGNHFVESDGTKEGNPQPPMKGELLLKAEGATLAGCGSSVGGALWPSG EASEAGRPPGLETYGPSPVTLISCQQGPAPRLEGSHCVEPEGNHFGNPQPSMDGEILLRAEGSTPAGGGLSSGGGFQPSG</p> <p>961 SLFASHLN SLFASHLN LAFASHVN</p> <p>968</p>
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FIG.8A

G	I	H	N	L	E	T	L	D	L	N	Y	N	K	I	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	ATC	AAG	GCC	120	
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GGG	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCC	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GCA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540

FIG.8B

S	I	H	P	E	A	F	S	T	L	H	S	L	V	K	L	D	L	T	D	200
TCC	ATC	CAC	CCT	GAG	GCC	TTC	TCC	ACC	CTG	CAC	TCC	CTG	GTC	AAG	CTG	GAC	CTG	ACA	GAC	600
N	Q	L	T	T	L	P	L	A	G	L	G	G	L	M	H	L	K	L	K	220
AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGA	CTT	GGG	GGC	TTC	ATG	CAT	CTG	AAG	CTC	AAA	660
G	N	L	A	L	S	Q	A	F	S	K	D	S	F	P	K	L	R	I	L	240
GGG	AAC	CTT	GCT	CTC	TCC	CAG	GCC	TTC	TCC	AAG	GAC	AGT	TTC	CCA	AAA	CTG	AGG	ATC	CTG	720
E	V	P	Y	A	Y	Q	C	C	P	Y	G	M	C	A	S	F	F	K	A	260
GAG	GTG	CCT	TAT	GCC	TAC	CAG	TGC	TGT	CCC	TAT	GGG	ATG	TGT	GCC	AGC	TTC	TTC	AAG	GCC	780
S	G	Q	W	E	A	E	D	L	H	L	D	D	E	E	S	S	R	R	P	280
TCT	GGG	CAG	TGG	GAG	GCT	GAA	GAC	CTT	CAC	CTT	GAT	GAT	GAG	GAG	TCT	TCA	AAA	AGG	CCC	840
L	G	L	L	A	R	Q	A	E	N	H	Y	D	Q	D	L	D	E	L	Q	300
CTG	GGC	CTC	CTT	GCC	AGA	CAA	GCA	GAG	AAC	CAC	TAT	GAC	CAG	GAC	CTG	GAT	GAG	CTC	CAG	900
L	E	M	E	D	S	K	P	H	P	S	V	Q	C	S	P	T	P	G	P	320
CTG	GAG	ATG	GAG	GAC	TCA	AAG	CCA	CAC	CCC	AGT	GTC	CAG	TGT	AGC	CCT	ACT	CCA	GGC	CCC	960
F	K	P	C	E	Y	L	F	E	S	W	G	I	R	L	A	V	W	A	I	340
TTC	AAG	CCC	TGT	GAG	TAC	CTC	TTT	GAA	AGC	TGG	GGC	ATC	CGC	CTG	GCC	GTG	TGG	GCC	ATC	1020
V	L	L	S	V	L	C	N	G	L	V	L	T	V	F	A	G	G	P	360	
GTG	TTC	CTC	TCC	GTG	CTG	CTC	TGC	AAT	GGA	CTG	GTG	CTG	CTG	ACC	GTG	TTC	GCT	GGG	CCT	1080

FIG. 8C

A	P	L	P	P	V	K	F	V	V	G	A	I	A	G	A	N	T	L	T	380
GCC	CCC	CTG	CCC	CCG	GTC	AAG	TTT	GTG	GTG	GCA	ATT	GCA	GCC	GCC	AAC	ACC	TTG	ACT	1140	
G	I	S	C	G	L	L	A	S	V	D	A	L	T	F	G	Q	F	S	E	400
GGC	ATT	TCC	TGT	GGC	CTT	CTA	GCC	TCA	GTC	GAT	GCC	CTG	ACC	TTT	GGT	CAG	TTC	TCT	GAG	1200
Y	G	A	R	W	E	T	G	L	G	C	R	A	T	G	F	L	A	V	L	420
TAC	GGA	GCC	CGC	TGG	GAG	ACG	GGG	CTA	GCC	TGC	CGG	GCC	ACT	GGC	TTC	CTG	GCA	GTA	CTT	1260
G	S	E	A	S	V	L	L	T	L	A	A	V	Q	C	S	V	S	V	440	
GGG	TCG	GAG	GCA	TCG	GTG	CTG	CTG	CTC	ACT	CTG	GCC	GCA	GTG	CAG	TGC	AGC	GTC	TCC	GTC	1320
S	C	V	R	A	Y	G	K	S	P	S	L	G	S	V	R	A	G	V	L	460
TCC	TGT	GTC	CGG	GCC	TAT	GGG	AAG	TCC	CCC	TCC	CTG	GGC	AGC	GTG	CGA	GCA	GGG	GTC	CTA	1380
G	C	L	A	L	A	G	L	A	A	A	L	P	L	A	S	V	G	E	Y	480
GGC	TGC	CTG	GCA	CTG	GCA	GGG	CTG	GCC	GCC	GCA	CTG	CCC	CTG	GCC	TCA	GTG	GCA	GAA	TAC	1440
G	A	S	P	L	C	L	P	Y	A	P	P	E	G	Q	P	A	A	L	G	500
GGG	GCC	TCC	CCA	CTC	TGC	CCC	TAC	GCG	CCA	CCT	GAG	GGT	CAG	CCA	GCA	GCC	CTG	GGC	1500	
F	T	V	A	L	V	M	M	N	S	F	C	F	L	V	V	A	G	A	Y	520
TTC	ACC	GTG	GCC	CTG	GTG	ATG	ATG	AAC	TCC	TTC	TGT	TTC	CTG	GTC	GTG	GCC	GGT	GCC	TAC	1560
I	K	L	Y	C	D	L	P	R	G	D	F	E	A	V	W	D	C	A	M	540
ATC	AAA	CTG	TAC	TGT	GAC	CTG	CCG	CGG	GGC	GAC	TTT	GAG	GCC	TGG	TGG	GAC	TGC	GCC	ATG	1620

FIG. 8D

V	R	H	V	A	W	L	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
CTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGG	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	CTA	1860
A	Y	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640	
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CCA	GGG	GCC	CCC	AGG	2040	
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720	
ATG	GAT	GGG	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTC	TCA	2160

FIG. 8E

G G G G F Q P S G I A F A S H V * 737
GGG GGT GGC GGC TTT CAG CCC TCT GGC TTG GGC TTT GCT TCA CAC GTG TAA 2211

ATATCCCTCCCCATTCTTCTCTCCCTCTCCCTTCCCTCTCTGGCTCCACTGACCTCTCCCTGTGA 2290

AATACAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAGTACCTGATCACCTCTCCCTGTGA 2369

CCATCACCAACGGGTGCCTCTGGCCTGGCTTCCCTCACGCTCACCTGATACTGGCCCTTCCCTTG 2448

TCATGTCGAAGCTGTGGACAGACCTGGACTTTTGACTTTTGCTTAAGGGAAATGAGGAAGTAAGACAGTGAAGGGG 2527

TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTCCCGTGTGACTCATG 2606

GATAGGATAACAAATGTGTTCCATGTACCATTAATCTGACATATGCCATGCATAAAGACTTCCATTAAATAAGCTT 2685

TGGAAAGAGATTAAAAAAAAAAAA 2711

FIG. 9

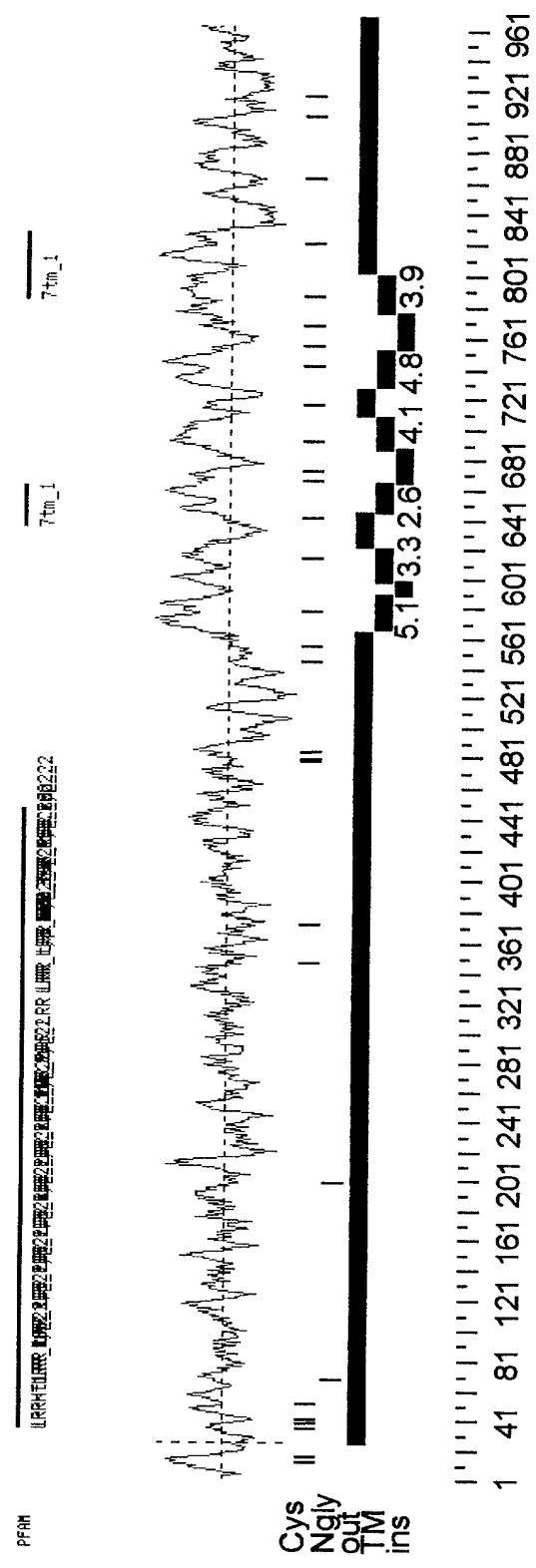


FIG. 10A

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
<u>LRR</u>	Leucine Rich Repeat	241.4	1.3e-68	16
<u>LRRNT</u>	Leucine rich repeat N-terminal domain	27.2	0.00038	1
<u>7tm_1</u>	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model Domain seq-f seq-t hmm-f hmm-t score E-value

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
LRRNT	1/1	34	65 ..	1	31 []	27.2	0.00038
LRR	1/16	67	90 ..	1	23 []	12.4	11
LRR	2/16	91	114 ..	1	23 []	24.2	0.0031
LRR	3/16	115	138 ..	1	23 []	19.9	0.062
LRR	4/16	139	162 ..	1	23 []	16.4	0.7
LRR	5/16	163	186 ..	1	23 []	27.5	0.00031
LRR	6/16	187	210 ..	1	23 []	12.1	13
LRR	7/16	211	234 ..	1	23 []	21.6	0.019
LRR	8/16	235	257 ..	1	23 []	18.2	0.2
LRR	9/16	258	281 ..	1	23 []	19.0	0.11
LRR	10/16	282	305 ..	1	23 []	10.2	32
LRR	11/16	306	328 ..	1	23 []	5.6	1.5e+02
LRR	12/16	329	352 ..	1	23 []	8.8	52
LRR	13/16	353	374 ..	1	23 []	19.2	0.097
LRR	14/16	375	398 ..	1	23 []	16.9	0.49
LRR	15/16	399	422 ..	1	23 []	23.7	0.0042
LRR	16/16	423	446 ..	1	23 []	16.4	0.66
7tm_1	1/2	635	662 ..	51	79 ..	3.4	2.2
7tm_1	2/2	784	827 ..	207	259 .]	1.1	11

FIG. 10B

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-

aCp++C+C +++ 1+ dCs++gL +vP dl

15088 34 ACPAPCHCQEgdIMLSADCSELGLS-AVPGDLD 65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

->nLeeLdLsnN.LtslppglfsnLp<-

+LdLs N+L+I pglf++L+

15088 67 LTAYLDLSMNNLTELQPGLFHHLR 90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

->nLeeLdLsnN.LtslppglfsnLp<-

LeeL+Ls+N+L+++p +fs+L

15088 91 FLEELRLSGNhlSHIPGQAFSGLY 114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ L L+nN+L ++p +++ Lp

15088 115 SLKILMLQNNqLGGIPAEALWELP 138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L+N ++ +p+ +f++L+

15088 139 SLQSLRLDANIISLVPERSFEGLS 162

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L+L++N Lt++p +++nLp

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13

->nLeeLdLsnN.LtslppglfsnLp<-

L+ L N+++++p+ +f+nL+

15088 187 ALQAMTLALNrISHIPDYAFQNLT 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019

->nLeeLdLsnN.LtslppglfsnLp<-

+L +L+L+nN+++++I ++f++L

15088 211 SLVVLHLHNNrIQHLGTHSFEGLH 234

FIG. 10C

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2

->nLeeLdLsnN.LtslppglfsnLp<-

nLe+LdL++N+L+++p +++ L

15088 235 NLETLDLNYNkLQEFPV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11

->nLeeLdLsnN.LtslppglfsnLp<-

+L+eL ++nN+++ +p+++f+ p

15088 258 RLQELGFHNNnIKAIPEKAFMGNP 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32

->nLeeLdLsnN.LtslppglfsnLp<-

L+++++ +N+++ + ++f+ Lp

15088 282 LLQTIHFYDNpIQFVGRSAFQYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02

->nLeeLdLsnN..LtslppglfsnLp<-

+L++L+L++ +++++p+ +++ +

15088 306 KLHTLSLNGAmdiQEFPD--LKGTT 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52

->nLeeLdLsnN.LtslppglfsnLp<-

+Le L L + +++ lp+g +++Lp

15088 329 SLEILTLTRAgIRLLPSGMQQLP 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097

->nLeeLdLsnN.LtslppglfsnLp<-

+L++L Ls+N++++lp+ +++ +

15088 353 RLRVLELSHNqIEELPS--LHRCQ 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49

->nLeeLdLsnN.LtslppglfsnLp<-

+Lee+ L++N++ ++ ++fs+L+

15088 375 KLEEIGLQHNrIWEIGADTFSQLS 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042

->nLeeLdLsnN.LtslppglfsnLp<-

+L+ LdLs N ++s++p++fs L

15088 399 SLQALDLSWNaiRSIHPEAFSTLH 422

FIG. 10D

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66

->nLeeLdLsnN.LtslppglfsnLp<-

+L +LdL +N+Lt+lp + +L

15088 423 SLVKLDLTDNqLTTLPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2

->dWpfGsalCkvtaldvvnmyaSillLta<-

+W G ++C+ +++l v++ aS+lLt+

15088 635 RWETG-LGCRATGFLAVLGSEASVLLTL 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11

*->lCWlPyfivllldtlc.lsimsstCelervlptallvtlwLayvNs

l+ P + + + +l ++ +++++++v l++ ++

15088 784 LLYCPVAFLSFASMLGIFPV-----

TPEAVKSVLLVVLPLPA 820

clNPiIY<-*

clNP++Y

15088 821 CLNPLLY 827

FIG. 11A

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Searching for complete domains in SMART
hhmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
HMM file: /ddm/robison/smart/smart.all.hmms
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184.seq

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrnt1		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lrrnt1	1/1	34	70	1	38	25.7	0.0011
LRR_PS_2	1/13	64	87	1	24	1.9	1.2e+02
LRR_typ_2	1/14	64	88	1	24	12.6	2.1

FIG. 11B

LRR_bac_2	1/7	89	108	..	1	24	[]	0.9	80
LRR_PS_2	2/13	89	111	..	1	24	[]	17.2	0.4
LRR_typ_2	2/14	89	112	..	1	24	[]	32.1	1.3e-05
LRR_RI_2	1/4	89	115	..	1	28	[]	3.6	14
LRR_bac_2	2/7	113	132	..	1	20	[]	1.6	66
LRR_PS_2	3/13	113	136	..	1	24	[]	1.1	1.5e+02
LRR_typ_2	3/14	113	136	..	1	24	[]	19.2	0.1
LRR_bac_2	3/7	137	156	..	1	20	[]	0.1	1e+02
LRR_PS_2	4/13	137	159	..	1	24	[]	7.1	24
LRR_typ_2	4/14	137	160	..	1	24	[]	25.9	0.00095
LRR_PS_2	5/13	161	183	..	1	24	[]	11.4	6.6
LRR_typ_2	5/14	161	184	..	1	24	[]	27.5	0.00031
LRR_sd22_2	1/5	161	187	..	1	22	[]	5.3	31
LRR_RI_2	2/4	161	190	..	1	28	[]	5.3	8
LRR_PS_2	6/13	185	207	..	1	24	[]	7.0	25
LRR_typ_2	6/14	185	208	..	1	24	[]	23.2	0.0062
LRR_PS_2	7/13	209	232	..	1	24	[]	3.1	79
LRR_typ_2	7/14	209	232	..	1	24	[]	28.1	0.0002
LRR_RI_2	3/4	209	235	..	1	28	[]	1.2	31
LRR_sd22_2	2/5	209	235	..	1	22	[]	13.5	3
LRR_bac_2	4/7	233	252	..	1	20	[]	10.7	4.1
LRR_typ_2	8/14	233	255	..	1	24	[]	16.1	0.76
LRR_PS_2	8/13	233	255	..	1	24	[]	17.1	0.43
LRR_bac_2	5/7	256	275	..	1	20	[]	0.2	1e+02
LRR_PS_2	9/13	256	278	..	1	24	[]	2.9	85
LRR_typ_2	9/14	256	279	..	1	24	[]	24.4	0.0026

FIG. 11C

LRR_typ_2	10/14	327	350	..	1	24	[]	3.1	29
LRR_bac_2	6/7	351	370	..	1	20	[]	14.6	1.3
LRR_PS_2	10/13	351	372	..	1	24	[]	10.8	8
LRR_sd22_2	3/5	351	372	..	1	22	[]	7.6	16
LRR_typ_2	11/14	351	373	..	1	24	[]	18.8	0.13
LRR_RI_2	4/4	351	378	..	1	28	[]	2.6	19
LRR_PS_2	11/13	373	396	..	1	24	[]	2.3	1e+02
LRR_typ_2	12/14	374	396	..	1	24	[]	6.8	10
LRR_sd22_2	4/5	397	418	..	1	22	[]	7.0	19
LRR_PS_2	12/13	397	419	..	1	24	[]	13.6	3.4
LRR_typ_2	13/14	397	420	..	1	24	[]	30.4	4.3e-05
LRR_bac_2	7/7	421	440	..	1	20	[]	5.8	18
LRR_sd22_2	5/5	421	441	..	1	22	[]	3.7	49
LRR_PS_2	13/13	421	442	..	1	24	[]	5.5	39
LRR_typ_2	14/14	421	444	..	1	24	[]	21.6	0.018

Alignments of top-scoring domains:

lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
 ->qCPapCtCsp.dfgtavVdcsgrgLttlevPldlPadtl<-
 +CPapC+C ++ ++ dCs+gL +vP d1 + t +
 15088 34 ACPAPCHCQEGIMLSADCSELGLS--AVPGDLDPLTAY

lrrnps2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
 ->ltSL.qvLdLsnNnLsGeIPssign<-
 L L+ +LdLs NnL+ e+ + 1+
 15088 64 LDPLTAYLDLMSNNLT-ELQPGFLFH

FIG. 11D

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
->LpnL.reLdLsnNqltsLPpgAFgg<-
L L+ LdLs N+Lt+L pg+F++
15088 64 LDPLTAYLDLSMNNNLTELQPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
->PpsLkeLnvsnNrLteLPeL<-
+L+eL+ S+N+L+ P
15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_ps_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
->LtsLqvLdLsnNnLsGeIPss1gn<-
L+ L+L+Ls+N+Ls +IP + ++
15088 89 LRFLEELRLSGNHLHS-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
->LpnLreLdLsnNqltsLPpgAFgg<-
L+ L+eL+Ls+N+L++P +aF+g
15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
->npsLreLdLsnNk1.gdeGaraLaeaLks<-
++ L+eL+Ls+N+L++G + ++L S
15088 89 LRFLEELRLSGNHLSHIPG--QAFSGLYS 115

FIG. 11E

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66

->PpsIkeLnvsnNrLteLPeL<-

SLk+L +nN+L P+

15088 113 LYSIKitMLQNNQLGGIPAE 132

LRR_ps_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02

->LtsLqvLdLsnNnLsGeIPss1gn<-

L sL++L L+nN+L G +1+

15088 113 LYSIKitMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1

->LpnLrLdLsnNqLtsLPPgaFqg<-

L +L+ L L+nNqL +P++a++

15088 113 LYSIKitMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02

->PpsIkeLnvsnNrLteLPeL<-

PSL++L+ + N ++ Pe

15088 137 LPSIQLSLRLDANLISLVPER 156

LRR_ps_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24

->LtsLqvLdLsnNnLsGeIPss1gn<-

L+sLq+L+L N +s +P+ +

15088 137 LPSIQLSLRLDANLIS-LVPERSSEE 159

FIG. 11F

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
->LpnLreLdLsnNqLtsLPPgaFqg<-
Lp+L++L+ N ++ +P++ F+g
LPSIQSLRLDANLISLVPERSFEG 160

LRR_ps_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
->LtsLqvLdLsnNnLsGeIPss1gn<-
L+sL++L L +N L+ eIP n
LSSLRHLWLDNNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
->LpnLreLdLsnNqLtsLPPgaFqg<-
L++Lr+L L++N+Lt++P +a+++
LSSLRHLWLDNNALTIEIPVRALNN 184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
->LtnLeeLdLsqNkI.....kkiENLde<-
L+ L++L+L +N +++ + + NL
LSSLRHLWLDNNALTieipvRALNNLPA 187

LRR_ri_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
->npsLreLdLsnNk1gdeGarAL..aealks<-
++sLr L+L +N 1++ +raL++ aL++
LSSLRHLWLDNNALTIEIPVRALnnLPALQA 190

FIG. 11G

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25

->LtsLqvLdLsnNnLsGeIPssign<-

15088	185	L+ Lq L+ N+s +IP+ ++	LPALQAMTLAINRIS-HIPDYAFQ	207
-------	-----	----------------------	--------------------------	-----

LRR_TYP_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062

->LpnLreLdLsnNqLtsLPpgaFqg<-

15088	185	Lp+L+ L N++++P+ aFq+ LPALQAMTLAINRISHIPDYAFQ	N	208
-------	-----	--	---	-----

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79

->LtsLqvLdLsnNnLsGeIPssign<-

15088	209	LtsL+vL+L+nN++ S+ ITSLVVVLHNNRIQHLGTHSEFG	232
-------	-----	---	-----

LRR_TYP_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002

->LpnLreLdLsnNqLtsLPpgaFqg<-

15088	209	L++L +L+L+nN++L F+g ITSLVVVLHNNRIQHLGTHSEFG	232
-------	-----	---	-----

LRR_TYP_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31

->npsLreLdLsnNk1gdeGaralaeaLks<-

15088	209	++sL +L+L NN + G + e+L+ ITSLVVVLHNNRIQHLGTHSE-EGLN	235
-------	-----	--	-----

FIG. 11H

LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
->ItnLeelldlsgNkI....KkiENLde<-
15088 209
LTSLWVLHLHNNRIGHLgTHSFEGLHN 235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
->PpsLkeLnvsnNrLtelPeL<-
++L++L+ ++N+L e+P
15088 233
LHNLETLDLNYNKLQEFPPVA 252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 10.7, E = 4.1
->LpnLreLdLsnNqLtsLPpgafFgg<-
L+nL++LdL++N+L++ P + +
15088 233
LHNLETLDLNYNKLQEFPPVAI-RT 255

LRR_ps_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
->LtsLqvLdLsnNnLsGeIPss1gn<-
L++L++LdL++N+N+L e+P +
15088 233
LHNLETLDLNYNKLQ-EFPVAlRT 255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
->PpsLkeLnvsnNrLtelPeL<-
+L+eL+ nN+++ Pe
15088 256
LGRLQELGFHNNNIKA1PEK 275

FIG. 11

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
->LtsLqvLdLsnNnLsGeIPss1gn<-
L +Lq+L +nNn+ IP+ +
LGRlQELGFHNNNIK-AIPEKAFM 278

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
->LpnLreLdLsnNqLtsLPpgafFqg<-
L+ L+eL +nN+++++P+ aF g
LGRlQELGFHNNNIKAIPEKAFMG 279

LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
->LpnLreLdLsnNqLtsLPpgafFqg<-
++L+ L L + ++ LP+g++q
TTSLEITLTTRAGIRLILPSGMCQQ 350

LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
->PpsLkeLnvsmNrLteLPeL<-
p+L+ L s+N++eLp L
IPLRLRVVLELSHQNQIEELPSL 370

LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
->LtsLqvLdLsnNnLsGeIPss1gn<-
L++L+vL+Ls+N++ e+Ps L +
IPLRLRVVLELSHQNQIE-ELPS-LHR 372

FIG. 11J

LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
->LtnLeelLsqNkikkienLde<-
L +L+L+Ls+N+I+ + L+
LPRLRVLELSSHNQIEELPSLHR 372

LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
->LpnLreelLsnNqltsLppgafEqg<-
Lp Lr+L Ls+Nq+++LP + ++
LPRLRVLELSSHNQIEELLP-SLHRC 373

LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
->npsLreelLsnNk1gdeGaralaeks<-
+p+Lr+L Ls+N + + ++ L++
LPRLRVLELSSHNQIEELPSLHRCQKLEE 378

LRR_ps_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
->LtsLqvLdLsnNnLsGeIPss1gn<-
++L++ L++N++ +++++
15088 373 CQKLEEIGLQHNRIWEIGADTFSQ 396

LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
->LpnLreelLsnNqltsLppgafEqg<-
+L+e L++N++ + ++F+
15088 374 -QKLEEIGLQHNRIWEIGADTFSQ 396

FIG. 11K

LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
->LtnLeeLdLsqNkikkienLde<-

15088	397	LSSLQALDLSWNNAIRSIHPEAF	418
-------	-----	-------------------------	-----

LRR_ps_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
->LtsLqvLdLsnNnLsGeIPss1gn<-

15088	397	LSSLQALDLSWNNAIR-SIHPEAFS	419
-------	-----	---------------------------	-----

LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
->LpnLreLdLsnNqLtsLPpgafqgq<-

15088	397	LSSLQALDLSWNNAIRSIHPEAFST	420
-------	-----	---------------------------	-----

LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
->PpsLkeLnvsnNrLteLPeL<-

15088	421	LHSLVKKLDLTDNQLTTLPLA	440
-------	-----	-----------------------	-----

LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
->LtnLeeLdLsqNkikkienLde<-

15088	421	LHSLVKKLDLTDNQLTTL-PLAG	441
-------	-----	-------------------------	-----

FIG. 11L

LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39

```
*->LtsLqvLdLsnNnLsGeIPss1gn<-*  
L+SL+ LdL +N+L+ ++P  
LHSLVKLDLTDNQLT-TLPL-AGL 442  
15088 421
```

LRR_TYP_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018

```
*->LpnLrelLdLsnNqLtsLPPgaFqg<-*  
L+L +LdL +NqL+LP ++g  
LHSLVKLDLTDNQLTTLPLAGLGG 444  
15088 421
```

//

FIG. 12A

GAP of: FrGcgManager_101_HTAUB3ha_ check: 2817 from: 1 to: 3637
mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_HTA0f1s0_ check: 3059 from: 1 to: 2711
corrected human LGR6 (analysis o - Import - complete

Symbol comparison table:
/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight:	12	Average Match:	10.000
Length Weight:	4	Average Mismatch:	0.000
Quality:	21826	Length:	3688
Ratio:	8.051	Gaps:	20
Percent Similarity:	84.248	Percent Identity:	84.211

Match display thresholds for the alignment(s) :

	=	IDENTITY
:	=	5
.	=	1

FIG. 12B

FrGcgManager_101_HTAUB3ha_x_FrGcgManager_101_ITAOFLSO_x

FIG. 12C

1151	ATCTTTGAAATGGTGCCTACTGATAATCCAAGAGTTCCAGACCTCAAAGGCCA	1200
237	ATCTCTGAAATGGTGCCTATGGACATTCAGGAGTTCCAGATCTCAAAGGCCA	286
1201	CCACTAGCCTGGAGATCCTGACCCCTGACCGTGGGGCATCAGACTGCTC	1250
337	CCACCAGCCTGGAGATCCTGACCCCTGACCGCAGGCATCCGGCTGCTC	336
1251	CCACCGGGAGTGTGCCAACAGCTTAGGCTCCGAATCCTGGAGCTGTC	1300
337	CCATCGGGGATGTGCCAACAGCTGCCAGGCTCCGAGTCCTGGAAACTGTC	386
1301	TCATAATCAGATCCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG	1350
387	TCACAATTGAGGAGCTGCCAGCCTGCACAGGTGTCAAGAAATTGG	436
1351	AGGAAATTGGCCTCCGACATAACAGGATCAAGGAATTGGTGCAGATAACC	1400
437	AGGAAATTGGCCTCCAACACAACCCGCATCTGGGAATTGGAGCTGACACCC	486
1401	TTAGCCAGCTGGCTCCTGGCAAGGCTTAACTGAGTTGGAATGCCAT	1450
487	TTAGCCAGCTGGCTCCCTGGCAAGGCCCTGGATCTTAGCTGGAAACGCCAT	536
1451	CCGTGCCATCCACCCCTGAGGCTTTCCTCAACCCCTTCGATCCCTGGTTAAGC	1500
537	CCGGTCCATCCACCCCTGAGGCCCTTCCTCCACCCCTGCAACTCCCTGGTCAAGC	586

FIG. 12D

FIG. 12E

1851	CAGTGAGGCCCTGTTCCAGGCCCTTCAAGGCCCTTGCGAGGACCTCTTTGA	1900
1901	GAGCTGGGCATCCGCCTTGCCTGTTGGCCATCGTGTGCTCTCCGTAC	1950
937	CAGTGTAGGCCCTACTCCAGGCCCTTCAAGGCCCTTGAGTAACCTCTTTGA	986
987	AAGCTGGGCATCCGCCTGGCCATGGCGTGTGGCTCTCCGTGC	1036
1951	TCTGTAACGGCTGGTGCTGACAGTCCTTGCCAGGGACCCAGCCCC	2000
1037	TCTGCAATGGACTGGTGGCTGACCCGTGTTGCTGGCGGGCTGCC	1086
2001	CTGTCCCCCGTCAAGCTTGTGGTGGGTGCAATGGCAGGGCCAAGGCCCT	2050
1087	CTGCCCCGGTCAAGTTGTGGTAGGTGGATTCAGTGCAAGGCCAACACCTT	1136
2051	GACGGGCATTCCCTGTGGCTCCCTGGCTCTGTGGACGGCTTGACCTATG	2100
1137	GACTGGCATTCCCTGTGGCTTCTAGCCTCAGTGGATGCCCTGACCTTTG	1186
2101	GTCAGTTGCTGAGTATGGAGGCCGCTGGGAGAGGGCTGGCTGGCTGCCAG	2150
1187	GTCAGTTCTGAGTACGGAGGCCGCTGGGAGACGGGCTAGGCTGGCTG	1236
2151	GCTACGGGCTTCCGGCTGTCTGGGTTAGGGCTGGCTGGTCTGGCTGCCAG	2200
1237	GCCACTGGCTTCCGGCAGTACTGGGTGGAGGCAATGGGTGGCTG	1286

FIG. 12F

2201	CACACTGGCGCCGTGCAGTGCAAGCATCTGTGACCTGTGCGTCCGGAGCCT	2250
11287	CACTCTGGCGCAGTGCAGTGGCAGCGTCCGGTGTCCGTCAGGCGCACTGGGATGC	1336
2251	ACGGGAAGGGGCCGTGGCAGCGTCCGGCAGGGCACTGGGATGC	2300
1387	ATGGGAAGTCCCCCTCCCTGGCAGCGTTGGCAGGCAAGGGTCTAGGCTGC	1386
2301	CTGGCGCTGGCGGGCTGGCCACTGCCGCTGGCCTCGGGCTCGGTGGGAGA	2350
1387	CTGGCACTGGCAGGGCTGGCCACTGCCCTGGCCTCAGTGGGAGA	1436
2351	GTATGGCGCCCTCCCACTCTGCCCTACGCCCTACGCCCTACGGGGCGGC	2400
1437	ATACGGGGCCTCCCACTCTGCCCTACGCCCTACGCCACCTGAGGGTCAGC	1486
2401	CGGCCGCCCTGGCTTCGCTGTAGGCCCTACATCAAGCTCTACTGTGACCTGCCACG	2450
1487	CAGCAGCCCTGGGCTTCAACCGTGGCCCTGCTGATGATGAACTCCTTCCTGT	1536
2451	TTCCCTGGTGGTGGCCCTACATCAAGCTCTACTGTGACCTGCCACG	2500
1537	TTCCCTGGTGGTGGCCCTACATCAAATGTAACCTGACCTGCCCTGCGCG	1586
2501	GGGTGACTTTGAGGCCGTTGGACTGGCCATGGTGGCCACGTGGCCT	2550
1587	GGGGGACTTTGAGGCCGTTGGGACTGGCCATGGTGGCCACGTGGCCT	1636

FIG. 12G

2551 GGCTCATCTTGGCAGATGGCTCCCTACTGCCCGTGGCCTCAGC 2600
1637 GGCTCATCTTCGCAAGCGGCTCCCTACTGTCGGCTGGCCTCAGC 1686

2601 TTTGCCTCCATGCTGGCCCTCTCCCTGTCACCCCCGAGGCTGTCAGTC 2650
1687 TTGCCTCCATGCTGGCCCTCTCCCTGTCACGCCCGAGGCCGTCAGTC 1736

2651 AGTCCCTCTGGTGGCTGCCTGCCTGCCTAACCCACTGCTCT 2700
1737 TGTCCCTGCTGGTGGCTGCCCTGCCTAACCCACTGCTGT 1786

2701 ACCTGCTCTCAACCCCTACTTCCGGATGACCTTGGCTCTGGCCA 2750
1787 ACCTGCTCTCAACCCCACTTCCGGATGACCTTGGCTTGCGGCC 1836

2751 AGCCCTCGGCCCCAGGGCCCTAGCCTACGCTGCAAGCCGGTGAAGCTGGA 2800
1887 CGGCAGGGACTCAGGGCCCTAGCCTATGCTGCGGGAGCTGGA 1886

2801 GAGAGCTCCTGCCGACTCCACCAAGGGCTGGCTGGCTTCTCAGATGTGG 2850
1887 GAGAGCTCCTGTTGATTCTACCCAGGCCCTGGTGAAGCTTCTGATGTGG 1936

2851 ATCTTATCTGGAAGCTTCTGAGGCTGGCAGGCCTCCTGGCTAGAGACC 2900
1937 ATCTCATCTGGAAAGCTTCTGAAGCTGGCCCCCTGGCTGGAGACC 1986

FIG. 12H

2901	TATGGCTTCCCTTCAGTGACCCTCATCTCCGACATCAGCCGGGCCAC	2950
1987	TATGGCTTCCCTTCAGTGACCCTCATCTCCGACATCAGCCGGGCCAC	2036
2951	CAGGCTGGAGGGAAACCATTATAGAGTCTGATGGAACCAAGTTGGGA	3000
2037	CAGGCTGGAGGGCAGGCCATTGTGTAGAGCCAGAGGGAAACCACTTGGGA	2086
3001	ACCCACAAACCTCCCATGAGGGAGAACTGCTGCTGAAGGCAAGGGAGGCC	3050
2087	ACCCCCAACCTCCATGGATGGAGAACCTGCTGCTGAAGGGAGGGATCT	2136
3051	ACTTTGGCAGGGCTGGCTCTTCCGTGGGGAGCCCTCTGGCCCTCTGG	3100
2137	ACGCCAGCAGGTGGAGGCTTGTCAAGGGGTGGCGGCTTCAGCCCTCTGG	2186
3101	CTCTCTCTTGCCTCTCACTTGTAAATAATCCCTCCATTCTCTCTCC	3133
2187	CTGGCCCTTGTGCTCACACGTGTAAATAATCCCTCCATTCTCTCC	2236
3134	CTCTGTTC...TGTC..CTCTCCCATC..CAATGATGGCTGCTTAA	3174
2237	CTCTCTCTTCCCTTCCCTCTGGTGAATGATGGCTTCTAA	2286
3175	AGGAAGACAACCTCAAAC	3212
2287	ACCAAAATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAG	2336

FIG. 121

FIG. 12J

3550	GCTGNGCCAAGTGTCTGTTAAATACACTTGGAAAGACATTGAAAA	3599
:		
2652	GCCATGCATAAGACTTCCTATTAAATAAGCTTGGAAAGAGATTAAAAA	2701
	.	.
3600	AAAAAAAGGGCGGCCGC	3637
2702	AAAAAAAAGGGCGGCCGC	2711

FIG. 13A

```
GAP of: FrGcgManager_102_MTA0uxMaE  check: 8470  from: 1  to: 968
mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAF7nc1_  check: 5092  from: 1  to: 737
corrected mLGR6.aa (analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
Matrix made by matblas from blosum62.ijj

Gap Weight: 12  Average Match: 2.778
Length Weight: 4  Average Mismatch: -2.248

Quality: 3424  Length: 968
Ratio: 4.646  Gaps: 0
Percent Similarity: 90.773  Percent Identity: 89.281

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1
```

FIG. 13B

FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_ntaaffnCl_ May 5, 19100 15:04

FIG. 13C

451 KGNIALSQAFSKDSEPKLRLILEVPIAYQCCAYGICASEFFKTSQGWQAEDF 500
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
220 KGNIALSQAFSKDSEPKLRLILEVPIAYQCCPYGMCASEFFKASGQWEAEDL 269

501 HPEEEAAPKRPLGLLAGQAEHNHYDLDLQMGTEDSKPNPSVQCSPPVPG 550
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
270 HLDDEESSKRPLGLLARQAEHNHYDQDLDELOQLEMEDSKPHPSVQCSPTPG 319

551 PEKPCCEHLEFWSGWIGRLAVWAIVLLSVLCNGLVLITVEASGPSPLSPVKLV 600
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
320 PEKPCCEYLFESWGWIGRLAVWAIVLLSVLCNGLVLITVFAGGPAPLPPVKFV 369

601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESEGLGCQATGFLAV 650
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
370 VGANIAGANTLTGISCGLLASVDALTFGQFSEYGARWEITGLGCRAATGFLAV 419

651 LGSEASVLLITIAAVQCSISVTCVRAYGKAPS PGSVRAGLGLAAGLA 700
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
420 LGSEASVLLITIAAVQCSVSVCVAYGKSPSLGGSVRAGVILGCLALAGLA 469

701 AALPLASVGEYGASPLCLPYAPPEGPRAALGFAVALVMMNLSCLFLVVAGA 750
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNNSFCFLVVAGA 519

751 YIKLYCDLPRGDFEEAVWDCCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
520 YIKLYCDLPRGDFEEAVWDCCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 569

FIG. 13D

801	FPVTPEAVKSVLVLVVLPLPACLNPLLYLLEFNLNPHFRRDLRRLWPSPRSPGGP	850
570	FPVTPEAVKSVLVLVVLPLPACLNPLLYLLEFNLNPHFRRDLRRLPRAFDGGP	619
851	LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT	900
620	LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT	669
901	LISRHQPGATRLEGNHFILESDGTFGNPQOPPMKGELLIKAEGATLAGCGS	950
670	LISCCQQPGAPRILEGSHCVEPEGNHFGNNEQPSMDGEILLRAEGSTPAGGGI	719
951	SVGGALMWPSGSILFASHL*	968
720	SGGGGFQPSGLAFAASHV*	737

FIG. 14A

FIG. 14B

FIG. 14C

AGGATGGCCCGAGTACCTGGCTCCACCTGATCACCTCTCCCTGTGACCATCACCAACGGGT
GCCCTCTTGGCTTGCCCTTCCCTTGGCTTCCCTCACCTTCAGCTTCACTTGTATACTGGGCCTCTTC
CTGTCTCATGTCTGAAGCTGTGGACCARAGACCTGGACTTTGTCTGCTTAAGGGAAATGA
GGAAAGTAAAGACAGTGAAGGGTGGAGGGTGGACTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAGGCCTGGAAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAATGIG
TTCCCATGACATTAATCTTGACATATGCCATAAACTTCCTTAAATAAGCT
TTGGAGAGATT

FIG. 15

>15088
MSPPPGLRALLCAALCASRRAGGAQPGPGPTACPAAPCHCQEDGIMIISADCSELGLSAVPGDLDPPLTAYLDLSMNLT
EIQPGLEFHHLBFLFELRLSGNHLSHIPQAFSGLYSLKILMIQNNQQLGGIPAELWELPSLQSLRLDANLISLVPERSF
EGLSSLRHLWIDDDNALTEIPVRALNNLPALQAMTLALNRI SHIPDYAFQNLITSLIVVLLHNNRIOHLGTHSSEGHLNLE
TLDLNYNKIQEFPVAIRTLGRILQELGFHNNNIKAIPPEKAFMGNPLLQTIHFYDNPPIQFVGRSAFQYLPKLHTLSSLNGAM
D1QEFPDLKGTTSLEIITRAGIRLIPSGMCQQLPRIRVYLELHSNOIIEELPSLHRCQKLEEIGLQHNRIWEIGADTES
QLSSLQALDLISWNAIRSIPEAFSTLHSVLRLDLDNQLTTLPLAGLGGIMHLKLGKGNLALSQAFSKDSEPKLRLIEVP
YAYQCCPYGMCAFFKASGQWEAEDLHIDDEESSKRPIGLLARQAENHYDQDLDLQLEMEDSKPHPSVQCSPTPGPFK
PCEYLFESWGIRLAVWAVLILSVLNGLVLITFAGGGAPLPPVKEVVGAIAGANTLTGISCGLIASVDALTEGQFSEY
GARWEITGLGCRATGFFLAVLGSEASVLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAAGLAAALPLASVGEY
GASPPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAAGAYIKIYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVA
FLSFAASMIGLFPTPEAVKSVLLVVLPLPACLNPLLYLFFNPHFRDDLRPRAFGDSGPLAYAAAGELEKSSCDSTQA
LVAFSDVDLILEASEAGRPPGLETYGEPSTLISQQQGAPRILESHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGG
GLSGGGGFQPSGLAFASHV*

FIG. 16A

protein alignment between mouse and human
> LGR6.

15088m (analysis only) - Import - complete

to: FrGcgManager_9_QBASD4iW_ check: 8637 from: 1 to: 968

15088h (analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matlab from blosum62.ijl

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248

Quality:	4495	Length:	968
Ratio:	4.653	Gaps:	2
Percent Similarity:	91.097	Percent Identity:	89.855

Match display thresholds for the alignment(s):

	= IDENTITY
:	= 2
.	= 1

FrGcgManager_9_PBAOKgkFJ x FrGcgManager_9_QBASD4iW_ March 15, 19101 15:24

FIG. 16B

FIG. 16C

351	LPRRLTIELSHNQIEELPSLHRCQKLEEEIGLRRHNRKEIGADTFSQLGSSL	400
351	LPRRLTIELSHNQIEELPSLHRCQKLEEEIGLRRHNRKEIGADTFSQLSSL	400
401	QALDLISWNNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPIAGLGLGMHLKL	450
401	QALDLISWNNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPIAGLGLGMHLKL	450
451	KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFTFKTSQQWQAEDF	500
451	KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASEFFKASQQWEAEDL	500
501	HPEEEAAPKRPILGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPPVG	550
501	HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG	550
551	PFKPCEHLLFESWGIRLAVWAIVLLSVLCNG.VILITVEASGPSPLSP.KLV	598
551	PFKPCEYLLFESWGIRLAVWAIVLLSVLCNGLIVLITVEAGGPAPLPPVKFV	600
599	VGAMAGANALTGISCGLLASVDAALTYGQFAEYCARWESGLGCQATGFLAV	648
601	VGAIAAGANTLTGISCGLLASVDAALTFGQFSEYCARWETIGCRAATGFLAV	650
649	LGSEASVLLTAAVQCSISVTCVRAYGKAPSPPGSVRAGALGCLALAGLA	698
651	LGSEASVLLTAAVQCSVSVSCVRAYGKSPSISGSVRAGVLGCLALAGLA	700

FIG. 16D

699	AALPLASVGEYGASPLCLPYAPPPEGRPAALGFAVALVMMNSLCETLVVAGA	748
701	AALPLASVGEYGASPLCLPYAPPPEGRPAALGFTVALVMMNSFCETLVVAGA	750
749	YIKLYCDLPRGDFFEAIVWDCCAMVRHVAWLIFADGGLYCPVAFLSEASMLGL	798
751	YIKLYCDLPRGDFFEAIVWDCCAMVRHVAWLIFADGGLYCPVAFLSEASMLGL	800
799	FPTVPEAVKSVLVLVVLPLPACLNPLLYLLENPHFRDDILRRLMPSPRSPPGP	848
801	FPTVPEAVKSVLVLVVLPLPACLNPLLYLLENPHFRDDILRRLPRAGDSGP	850
849	LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSTV	898
851	LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSTV	900
899	LISRHQPGATRIEGNHFILESDGTTKFGNPQPPMKGELLLKAEGATLAGCGS	948
901	LISCOOPQGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL	950
949	SVGGALWPSGSILFASHL* 966	
951	SGGGGFQPSGLAFA SHV* 968	